



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 182689

TO: Juliet Switzer
Location: REM/2A61/2C70
Art Unit: 1634
Thursday, March 23, 2006
Case Serial Number: 10/633659

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

Juliet,

For the standard searches⁽²⁸³⁾, I gave you a 500 alignments or all 100% matches, whichever was fewer, so several results files have no hits. We don't have the ability to set the parameters as e.g. "all 100% matches, or 45 scores/15 alignments, whichever is greater".

For the score over length results:

ge.res = GenBank/EMBL
ngp.res = N. Geneseg
iss.res = Issued - Patents - NA
pubmain.res = Published - Applications - NA - Main
pubnew.res = " " " - New

There were no suitable hits in the EST database, so no EST results are included here.

Barb

From: Switzer, Juliet
Sent: Monday, March 20, 2006 4:44 PM
To: STIC-Biotech/ChemLib
Subject: please search

For 10/633659

please search the following:

1. SEQ ID NO 1
2. Nucleotides 441-455 of each of seq id no 1, seq id no 2, seq id no 3, and seq id no 4; please print at least all 100% hits
3. Nucleotides 449-459 of each of seq id no 1, seq id no 2, seq id no 3, and seq id no 4; please print at least all 100% hits
4. Please do a score/length search of nucleotides 426-485 of seq id no 1, wherein position 455 is an N, and sequence length is 12 nucleotides to 60 nucleotides and the score over length value is 80%.

please return results on disk.

THANKS.

Juliet Switzer
Art Unit 1634
phone: 571-272-0753
office: Remsen 2A61
mailbox: 2C70

RECEIVED
MAR 20 2006
STIC/CHEN, J
RECEIVED
MAR 20 2006
STIC/CHEN, J

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 80%, *length 12-60 nt*

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2006, 15:39:32 ; Search time 0.001 Seconds
 (without alignments)
 11.040 Million cell updates/sec

Title: US-10-633-659-1-N455
 Perfect score: 59
 Sequence: 1 cggggccaggagctaggttt.....ccctcagcacagggtctgtg 60

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 0.5

Searched: 5 seqs, 92 residues

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 5 summaries

Database : pubnewdb:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
c	1	15.8	26.8	19	1	US-11-101-244-1122053	Sequence 1122053,
	2	15.8	26.8	19	1	US-11-083-784-1122053	Sequence 1122053,
	3	15.4	26.1	18	1	US-10-310-914A-149256	Sequence 149256,
	4	15.4	26.1	18	1	US-10-310-914A-576667	Sequence 576667,
	5	15	25.4	18	1	US-10-310-914A-1337481	Sequence 1337481,

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2006, 15:42:31 ; Search time 0.001 Seconds
(without alignments)
178.320 Million cell updates/sec

Title: US-10-633-659-1-N455
Perfect score: 59
Sequence: 1 cggggccaggagctaggttt.....ccctcagcacagggtctgtg 60

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 106 seqs, 1486 residues

Total number of hits satisfying chosen parameters: 212

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 106 summaries

Database : pubmaindb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	33.9	20	1	US-10-239-176-9	Sequence 9, Appli
2	18	30.5	19	1	US-10-070-415A-22	Sequence 22, Appl
3	18	30.5	19	1	US-10-070-415A-23	Sequence 23, Appl
4	18	30.5	19	1	US-10-070-415A-24	Sequence 24, Appl
5	18	30.5	19	1	US-10-070-415A-25	Sequence 25, Appl
6	15	25.4	16	1	US-09-813-031-5	Sequence 5, Appli
7	15	25.4	16	1	US-09-813-031-6	Sequence 6, Appli
8	15	25.4	16	1	US-09-813-031-7	Sequence 7, Appli
9	15	25.4	16	1	US-09-813-031-8	Sequence 8, Appli
c 10	15	25.4	16	1	US-09-813-031-13	Sequence 13, Appl
c 11	15	25.4	16	1	US-09-813-031-14	Sequence 14, Appl
c 12	15	25.4	16	1	US-09-813-031-15	Sequence 15, Appl
c 13	15	25.4	16	1	US-09-813-031-16	Sequence 16, Appl
14	15	25.4	16	1	US-09-813-990A-5	Sequence 5, Appli
15	15	25.4	16	1	US-09-813-990A-6	Sequence 6, Appli
16	15	25.4	16	1	US-09-813-990A-7	Sequence 7, Appli
17	15	25.4	16	1	US-09-813-990A-8	Sequence 8, Appli
c 18	15	25.4	16	1	US-09-813-990A-13	Sequence 13, Appl

c	19	15	25.4	16	1	US-09-813-990A-14	Sequence 14, Appl
c	20	15	25.4	16	1	US-09-813-990A-15	Sequence 15, Appl
c	21	15	25.4	16	1	US-09-813-990A-16	Sequence 16, Appl
	22	15	25.4	16	1	US-10-633-659-5	Sequence 5, Appli
	23	15	25.4	16	1	US-10-633-659-6	Sequence 6, Appli
	24	15	25.4	16	1	US-10-633-659-7	Sequence 7, Appli
	25	15	25.4	16	1	US-10-633-659-8	Sequence 8, Appli
c	26	15	25.4	16	1	US-10-633-659-13	Sequence 13, Appl
c	27	15	25.4	16	1	US-10-633-659-14	Sequence 14, Appl
c	28	15	25.4	16	1	US-10-633-659-15	Sequence 15, Appl
c	29	15	25.4	16	1	US-10-633-659-16	Sequence 16, Appl
	30	14	23.7	15	1	US-10-070-415A-27	Sequence 27, Appl
	31	14	23.7	15	1	US-10-070-415A-28	Sequence 28, Appl
	32	14	23.7	15	1	US-10-070-415A-29	Sequence 29, Appl
	33	14	23.7	15	1	US-10-239-175-2	Sequence 2, Appli
	34	14	23.7	15	1	US-10-239-175-3	Sequence 3, Appli
	35	14	23.7	15	1	US-10-239-175-4	Sequence 4, Appli
c	36	12.8	21.7	16	1	US-10-730-771-222	Sequence 222, App
	37	12	20.3	15	1	US-09-825-805-137	Sequence 137, App
	38	11.4	19.3	13	1	US-10-257-017B-59693	Sequence 59693, A
c	39	11.4	19.3	13	1	US-10-257-017B-59694	Sequence 59694, A
	40	11.4	19.3	13	1	US-10-257-017B-64203	Sequence 64203, A
c	41	11.4	19.3	13	1	US-10-257-017B-64204	Sequence 64204, A
	42	11.4	19.3	13	1	US-10-257-017B-203399	Sequence 203399,
c	43	11.4	19.3	13	1	US-10-257-017B-203400	Sequence 203400,
	44	11.4	19.3	13	1	US-10-257-017B-207697	Sequence 207697,
c	45	11.4	19.3	13	1	US-10-257-017B-207698	Sequence 207698,
c	46	11	18.6	12	1	US-10-257-017B-313668	Sequence 313668,
	47	11	18.6	13	1	US-09-825-805-136	Sequence 136, App
	48	11	18.6	13	1	US-10-257-017B-35763	Sequence 35763, A
c	49	11	18.6	13	1	US-10-257-017B-35764	Sequence 35764, A
	50	11	18.6	13	1	US-10-257-017B-44169	Sequence 44169, A
c	51	11	18.6	13	1	US-10-257-017B-44170	Sequence 44170, A
	52	11	18.6	13	1	US-10-257-017B-88169	Sequence 88169, A
c	53	11	18.6	13	1	US-10-257-017B-88170	Sequence 88170, A
	54	11	18.6	13	1	US-10-257-017B-88337	Sequence 88337, A
c	55	11	18.6	13	1	US-10-257-017B-88338	Sequence 88338, A
	56	11	18.6	13	1	US-10-257-017B-111041	Sequence 111041,
c	57	11	18.6	13	1	US-10-257-017B-111042	Sequence 111042,
	58	11	18.6	13	1	US-10-257-017B-111043	Sequence 111043,
c	59	11	18.6	13	1	US-10-257-017B-111044	Sequence 111044,
	60	11	18.6	13	1	US-10-257-017B-129983	Sequence 129983,
c	61	11	18.6	13	1	US-10-257-017B-129984	Sequence 129984,
	62	11	18.6	13	1	US-10-257-017B-137951	Sequence 137951,
c	63	11	18.6	13	1	US-10-257-017B-137952	Sequence 137952,
	64	10.4	17.6	12	1	US-10-257-017B-289059	Sequence 289059,
	65	10.4	17.6	12	1	US-10-257-017B-295429	Sequence 295429,
c	66	10.4	17.6	12	1	US-10-257-017B-297067	Sequence 297067,
c	67	10.4	17.6	12	1	US-10-257-017B-302428	Sequence 302428,
c	68	10.4	17.6	12	1	US-10-257-017B-302429	Sequence 302429,
c	69	10.4	17.6	12	1	US-10-257-017B-303888	Sequence 303888,
	70	10.4	17.6	12	1	US-10-257-017B-334462	Sequence 334462,
c	71	10.4	17.6	12	1	US-10-257-017B-339313	Sequence 339313,
c	72	10.4	17.6	12	1	US-10-257-017B-344864	Sequence 344864,
	73	10.4	17.6	12	1	US-10-257-017B-356640	Sequence 356640,
c	74	10.4	17.6	12	1	US-10-257-017B-370259	Sequence 370259,
	75	10.4	17.6	13	1	US-10-257-017B-1097	Sequence 1097, Ap

c	76	10.4	17.6	13	1	US-10-257-017B-1098	Sequence 1098, Ap
	77	10.4	17.6	13	1	US-10-257-017B-38151	Sequence 38151, A
c	78	10.4	17.6	13	1	US-10-257-017B-38152	Sequence 38152, A
	79	10.4	17.6	13	1	US-10-257-017B-43939	Sequence 43939, A
c	80	10.4	17.6	13	1	US-10-257-017B-43940	Sequence 43940, A
	81	10.4	17.6	13	1	US-10-257-017B-46647	Sequence 46647, A
c	82	10.4	17.6	13	1	US-10-257-017B-46648	Sequence 46648, A
	83	10.4	17.6	13	1	US-10-257-017B-46821	Sequence 46821, A
c	84	10.4	17.6	13	1	US-10-257-017B-46822	Sequence 46822, A
	85	10.4	17.6	13	1	US-10-257-017B-72563	Sequence 72563, A
c	86	10.4	17.6	13	1	US-10-257-017B-72564	Sequence 72564, A
	87	10.4	17.6	13	1	US-10-257-017B-80605	Sequence 80605, A
c	88	10.4	17.6	13	1	US-10-257-017B-80606	Sequence 80606, A
	89	10.4	17.6	13	1	US-10-257-017B-103113	Sequence 103113,
c	90	10.4	17.6	13	1	US-10-257-017B-103114	Sequence 103114,
	91	10.4	17.6	13	1	US-10-257-017B-124375	Sequence 124375,
c	92	10.4	17.6	13	1	US-10-257-017B-124376	Sequence 124376,
	93	10.4	17.6	13	1	US-10-257-017B-127819	Sequence 127819,
c	94	10.4	17.6	13	1	US-10-257-017B-127820	Sequence 127820,
	95	10.4	17.6	13	1	US-10-257-017B-131261	Sequence 131261,
c	96	10.4	17.6	13	1	US-10-257-017B-131262	Sequence 131262,
	97	10.4	17.6	13	1	US-10-257-017B-138877	Sequence 138877,
c	98	10.4	17.6	13	1	US-10-257-017B-138878	Sequence 138878,
	99	10.4	17.6	13	1	US-10-257-017B-189283	Sequence 189283,
c	100	10.4	17.6	13	1	US-10-257-017B-189284	Sequence 189284,
	101	10.4	17.6	13	1	US-10-257-017B-207277	Sequence 207277,
c	102	10.4	17.6	13	1	US-10-257-017B-207278	Sequence 207278,
	103	10.4	17.6	13	1	US-10-257-017B-211199	Sequence 211199,
c	104	10.4	17.6	13	1	US-10-257-017B-211200	Sequence 211200,
	105	10.4	17.6	13	1	US-10-257-017B-221507	Sequence 221507,
c	106	10.4	17.6	13	1	US-10-257-017B-221508	Sequence 221508,

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2006, 15:41:24 ; Search time 0.001 Seconds
(without alignments)
238.320 Million cell updates/sec

Title: US-10-633-659-1-N455
Perfect score: 59
Sequence: 1 cggggccaggagctaggttt.....ccctcagcacagggtctgtg 60

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 140 seqs, 1986 residues

Total number of hits satisfying chosen parameters: 280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 141 summaries

Database : ngsdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	40	67.8	46	1	ADL92258	Human MxA gene PCR
2	20	33.9	20	1	ADJ87116	Nucleotide sequenc
3	20	33.9	20	1	ADL92245	Human MxA gene det
4	20	33.9	20	1	ADT02379	Target nucleotide
5	20	33.9	20	1	ADW92006	Forward direction
6	18	30.5	19	1	ABX08688	Pathogenic organis
7	18	30.5	19	1	ABX08689	Pathogenic organis
8	18	30.5	19	1	ABX08691	Pathogenic organis
9	18	30.5	19	1	ABX08690	Pathogenic organis
c 10	15	25.4	16	1	AAI70386	MxA gene promoter
11	15	25.4	16	1	AAI70379	Human MxA gene pro
12	15	25.4	16	1	AAI70380	Human MxA gene pro
c 13	15	25.4	16	1	AAI70387	MxA gene promoter
14	15	25.4	16	1	AAI70377	Human MxA gene pro
c 15	15	25.4	16	1	AAI70388	MxA gene promoter
c 16	15	25.4	16	1	AAI70385	MxA gene promoter
17	15	25.4	16	1	AAI70378	Human MxA gene pro
c 18	15	25.4	16	1	AAI70365	Human MxA gene pro

c	19	15	25.4	16	1	AAI70364	Human MxA gene pro
	20	15	25.4	16	1	AAI70355	Human MxA gene pro
	21	15	25.4	16	1	AAI70354	Human MxA gene pro
	22	15	25.4	16	1	AAI70356	Human MxA gene pro
c	23	15	25.4	16	1	AAI70363	Human MxA gene pro
	24	15	25.4	16	1	AAI70357	Human MxA gene pro
c	25	15	25.4	16	1	AAI70362	Human MxA gene pro
	26	14	23.7	15	1	ABX08695	Pathogenic organis
	27	14	23.7	15	1	ABX08693	Pathogenic organis
	28	14	23.7	15	1	ABX08694	Pathogenic organis
	29	14	23.7	15	1	ABX08696	Pathogenic organis
	30	14	23.7	15	1	ADL72196	Human nucleotide s
	31	14	23.7	15	1	ADL72195	Human nucleotide s
	32	14	23.7	15	1	ADL72197	Human nucleotide s
	33	14	23.7	15	1	ADM30871	Escherichia coli n
	34	14	23.7	15	1	ADM30869	Escherichia coli n
c	35	14	23.7	15	1	ADM79790	Human DNA oligo pr
	36	14	23.7	15	1	ADO78065	Human MxA gene pro
	37	14	23.7	15	1	ADO78066	Human MxA gene pro
	38	14	23.7	15	1	ADT02370	Target nucleotide
	39	14	23.7	15	1	ADT02371	Target nucleotide
c	40	14	23.7	15	1	ADW92012	Nucleic acid G-pro
c	41	14	23.7	15	1	ADW92013	Nucleic acid T-pro
c	42	14	23.7	15	1	ADY97397	Target nucleic aci
c	43	14	23.7	15	1	ADY97396	Target nucleic aci
c	44	14	23.7	15	1	ADZ58672	Novel existence ra
c	45	14	23.7	15	1	ADZ58671	Novel existence ra
	46	13.4	22.7	15	1	ADR74748	Allele specific pr
	47	13	22.0	14	1	ADO78064	Human MxA gene pro
c	48	13	22.0	46	1	ADL92258	Human MxA gene PCR
c	49	12.8	21.7	16	1	AAC73325	Forward primer #64
	50	12.4	21.0	15	1	ADR74749	Allele specific pr
	51	12	20.3	15	1	ADV20455	Human anti-Her2 NC
	52	12	20.3	15	1	ADV36276	Human anti-HER2 NC
	53	12	20.3	15	1	ADV36277	Human anti-HER2 NC
	54	12	20.3	15	1	ADV63407	Human Her2 class I
c	55	12	20.3	15	1	AAS16192	Human apolipoprote
c	56	11.4	19.3	13	1	ABC59677	Oligonucleotide SE
	57	11.4	19.3	13	1	ABC64186	Oligonucleotide SE
c	58	11.4	19.3	13	1	ABH07721	Oligonucleotide SE
	59	11.4	19.3	13	1	ABC59676	Oligonucleotide SE
	60	11.4	19.3	13	1	ABH03422	Oligonucleotide SE
c	61	11.4	19.3	13	1	ABC64187	Oligonucleotide SE
c	62	11.4	19.3	13	1	ABH03423	Oligonucleotide SE
	63	11.4	19.3	13	1	ABH07720	Oligonucleotide SE
	64	11.4	19.3	14	1	AAV92803	Human A-raf target
c	65	11	18.6	12	1	ABI13695	Oligonucleotide pr
	66	11	18.6	13	1	ABC44152	Oligonucleotide SE
c	67	11	18.6	13	1	ABC35747	Oligonucleotide SE
	68	11	18.6	13	1	ABF37954	Oligonucleotide SE
	69	11	18.6	13	1	ABF11046	Oligonucleotide SE
	70	11	18.6	13	1	ABF29986	Oligonucleotide SE
	71	11	18.6	13	1	ABC35746	Oligonucleotide SE
c	72	11	18.6	13	1	ABF11045	Oligonucleotide SE
c	73	11	18.6	13	1	ABF11047	Oligonucleotide SE
c	74	11	18.6	13	1	ABC88153	Oligonucleotide SE
	75	11	18.6	13	1	ABF11044	Oligonucleotide SE

c	76	11	18.6	13	1	ABC44153	Oligonucleotide SE
c	77	11	18.6	13	1	ABF37955	Oligonucleotide SE
c	78	11	18.6	13	1	ABC88321	Oligonucleotide SE
c	79	11	18.6	13	1	ABF29987	Oligonucleotide SE
	80	11	18.6	13	1	ABC88152	Oligonucleotide SE
	81	11	18.6	13	1	ABC88320	Oligonucleotide SE
	82	11	18.6	13	1	ADV63406	Human Her2 class I
	83	10.4	17.6	12	1	AAA10344	DNA ligand binding
c	84	10.4	17.6	12	1	ABI44891	Oligonucleotide pr
c	85	10.4	17.6	12	1	ABI02455	Oligonucleotide pr
	86	10.4	17.6	12	1	ABH89066	Oligonucleotide pr
	87	10.4	17.6	12	1	ABI34489	Oligonucleotide pr
	88	10.4	17.6	12	1	ABH95436	Oligonucleotide pr
c	89	10.4	17.6	12	1	ABI03915	Oligonucleotide pr
c	90	10.4	17.6	12	1	ABH97074	Oligonucleotide pr
c	91	10.4	17.6	12	1	ABI39340	Oligonucleotide pr
c	92	10.4	17.6	12	1	ABI70286	Oligonucleotide pr
	93	10.4	17.6	12	1	ABI56667	Oligonucleotide pr
c	94	10.4	17.6	12	1	ABI02456	Oligonucleotide pr
	95	10.4	17.6	12	1	ABK70576	Ligand binding aff
	96	10.4	17.6	12	1	AAD45586	Competitor oligo c
	97	10.4	17.6	13	1	ABC72546	Oligonucleotide SE
c	98	10.4	17.6	13	1	ABC80589	Oligonucleotide SE
	99	10.4	17.6	13	1	ABF27822	Oligonucleotide SE
c	100	10.4	17.6	13	1	ABC01107	Oligonucleotide SE
	101	10.4	17.6	13	1	ABH21530	Oligonucleotide SE
c	102	10.4	17.6	13	1	ABC46805	Oligonucleotide SE
	103	10.4	17.6	13	1	ABC80588	Oligonucleotide SE
	104	10.4	17.6	13	1	ABH11222	Oligonucleotide SE
c	105	10.4	17.6	13	1	ABC72547	Oligonucleotide SE
	106	10.4	17.6	13	1	ABC01106	Oligonucleotide SE
c	107	10.4	17.6	13	1	ABC46631	Oligonucleotide SE
	108	10.4	17.6	13	1	ABF03116	Oligonucleotide SE
c	109	10.4	17.6	13	1	ABC38135	Oligonucleotide SE
	110	10.4	17.6	13	1	ABC46804	Oligonucleotide SE
	111	10.4	17.6	13	1	ABF31264	Oligonucleotide SE
c	112	10.4	17.6	13	1	ABF24379	Oligonucleotide SE
c	113	10.4	17.6	13	1	ABF27823	Oligonucleotide SE
	114	10.4	17.6	13	1	ABF89286	Oligonucleotide SE
	115	10.4	17.6	13	1	ABC38134	Oligonucleotide SE
	116	10.4	17.6	13	1	ABC43922	Oligonucleotide SE
c	117	10.4	17.6	13	1	ABF03117	Oligonucleotide SE
	118	10.4	17.6	13	1	ABH07300	Oligonucleotide SE
c	119	10.4	17.6	13	1	ABC43923	Oligonucleotide SE
c	120	10.4	17.6	13	1	ABF31265	Oligonucleotide SE
	121	10.4	17.6	13	1	ABF38880	Oligonucleotide SE
c	122	10.4	17.6	13	1	ABH11223	Oligonucleotide SE
c	123	10.4	17.6	13	1	ABF89287	Oligonucleotide SE
	124	10.4	17.6	13	1	ABF24378	Oligonucleotide SE
c	125	10.4	17.6	13	1	ABF38881	Oligonucleotide SE
c	126	10.4	17.6	13	1	ABH07301	Oligonucleotide SE
	127	10.4	17.6	13	1	ABC46630	Oligonucleotide SE
c	128	10.4	17.6	13	1	ABH21531	Oligonucleotide SE
	129	10.4	17.6	13	1	AAS16040	Human Ext2 polymor
	130	10.4	17.6	13	1	ABX10150	Human TIGR/Myocili
c	131	10	16.9	12	1	ABI21398	Oligonucleotide pr
c	132	10	16.9	12	1	ABI09503	Oligonucleotide pr

	133	10	16.9	12	1	ABI52103	Oligonucleotide pr
c	134	10	16.9	12	1	ABI78619	Oligonucleotide pr
	135	10	16.9	12	1	ABI02398	Oligonucleotide pr
	136	10	16.9	12	1	ABI11213	Oligonucleotide pr
	137	10	16.9	12	1	ABH86617	Oligonucleotide pr
	138	10	16.9	12	1	ABH76767	Oligonucleotide pr
c	139	10	16.9	12	1	ABH68372	Oligonucleotide pr
c	140	10	16.9	12	1	ABH90265	Oligonucleotide pr
c	141	10	16.9	12	1	ADZ85129	MODY 3 diabetes-as

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2006, 15:38:11 ; Search time 0.001 Seconds
(without alignments)
40.320 Million cell updates/sec

Title: US-10-633-659-1-N455
Perfect score: 59
Sequence: 1 cggggccaggagctaggttt.....ccctcagcacagggtctgtg 60

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 22 seqs, 336 residues

Total number of hits satisfying chosen parameters: 44

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 22 summaries

Database : issdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	15	25.4	16	1	US-09-813-031-5	Sequence 5, Appli	
2	15	25.4	16	1	US-09-813-031-6	Sequence 6, Appli	
3	15	25.4	16	1	US-09-813-031-7	Sequence 7, Appli	
4	15	25.4	16	1	US-09-813-031-8	Sequence 8, Appli	
c 5	15	25.4	16	1	US-09-813-031-13	Sequence 13, Appl	
c 6	15	25.4	16	1	US-09-813-031-14	Sequence 14, Appl	
c 7	15	25.4	16	1	US-09-813-031-15	Sequence 15, Appl	
c 8	15	25.4	16	1	US-09-813-031-16	Sequence 16, Appl	
9	15	25.4	16	1	US-09-813-990A-5	Sequence 5, Appli	
10	15	25.4	16	1	US-09-813-990A-6	Sequence 6, Appli	
11	15	25.4	16	1	US-09-813-990A-7	Sequence 7, Appli	
12	15	25.4	16	1	US-09-813-990A-8	Sequence 8, Appli	
c 13	15	25.4	16	1	US-09-813-990A-13	Sequence 13, Appl	
c 14	15	25.4	16	1	US-09-813-990A-14	Sequence 14, Appl	
c 15	15	25.4	16	1	US-09-813-990A-15	Sequence 15, Appl	
c 16	15	25.4	16	1	US-09-813-990A-16	Sequence 16, Appl	
17	12	20.3	15	1	US-09-474-432B-137	Sequence 137, App	
18	12	20.3	15	1	US-09-476-387-137	Sequence 137, App	

19	11	18.6	13	1	US-09-474-432B-136	Sequence 136, App
20	11	18.6	13	1	US-09-476-387-136	Sequence 136, App
21	10.4	17.6	12	1	US-09-393-783A-27	Sequence 27, Appl
22	10.4	17.6	12	1	US-09-151-890B-27	Sequence 27, Appl

OM nucleic - nucleic search, using sw model

Run on: March 23, 2006, 15:40:29 ; Search time 0.001 Seconds
 (without alignments)
 105.600 Million cell updates/sec

Title: US-10-633-659-1-N455
 Perfect score: 59
 Sequence: 1 cggggccaggagctaggttt.....ccctcagcacagggtctgtg 60

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 0.5

Searched: 55 seqs, 880 residues

Total number of hits satisfying chosen parameters: 110

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 55 summaries

Database : gedb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	30.5	19	1	BD178516	ACCESSION:BD178516
2	18	30.5	19	1	BD178517	ACCESSION:BD178517
3	18	30.5	19	1	BD178518	ACCESSION:BD178518
4	18	30.5	19	1	BD178519	ACCESSION:BD178519
5	18	30.5	19	1	BD182909	ACCESSION:BD182909
6	18	30.5	19	1	BD182910	ACCESSION:BD182910
7	18	30.5	19	1	BD182911	ACCESSION:BD182911
8	18	30.5	19	1	BD182912	ACCESSION:BD182912
9	15	25.4	16	1	BD090455	ACCESSION:BD090455
10	15	25.4	16	1	BD090456	ACCESSION:BD090456
11	15	25.4	16	1	BD090457	ACCESSION:BD090457
12	15	25.4	16	1	BD090458	ACCESSION:BD090458
c 13	15	25.4	16	1	BD090463	ACCESSION:BD090463
c 14	15	25.4	16	1	BD090464	ACCESSION:BD090464
c 15	15	25.4	16	1	BD090465	ACCESSION:BD090465
c 16	15	25.4	16	1	BD090466	ACCESSION:BD090466
17	15	25.4	16	1	BD090750	ACCESSION:BD090750

	18	15	25.4	16	1	BD090751	ACCESSION:BD090751
	19	15	25.4	16	1	BD090752	ACCESSION:BD090752
	20	15	25.4	16	1	BD090753	ACCESSION:BD090753
C	21	15	25.4	16	1	BD090758	ACCESSION:BD090758
C	22	15	25.4	16	1	BD090759	ACCESSION:BD090759
C	23	15	25.4	16	1	BD090760	ACCESSION:BD090760
C	24	15	25.4	16	1	BD090761	ACCESSION:BD090761
	25	15	25.4	16	1	AR441765	ACCESSION:AR441765
	26	15	25.4	16	1	AR441766	ACCESSION:AR441766
	27	15	25.4	16	1	AR441767	ACCESSION:AR441767
	28	15	25.4	16	1	AR441768	ACCESSION:AR441768
C	29	15	25.4	16	1	AR441773	ACCESSION:AR441773
C	30	15	25.4	16	1	AR441774	ACCESSION:AR441774
C	31	15	25.4	16	1	AR441775	ACCESSION:AR441775
C	32	15	25.4	16	1	AR441776	ACCESSION:AR441776
	33	15	25.4	16	1	AR577625	ACCESSION:AR577625
	34	15	25.4	16	1	AR577626	ACCESSION:AR577626
	35	15	25.4	16	1	AR577627	ACCESSION:AR577627
	36	15	25.4	16	1	AR577628	ACCESSION:AR577628
C	37	15	25.4	16	1	AR577633	ACCESSION:AR577633
C	38	15	25.4	16	1	AR577634	ACCESSION:AR577634
C	39	15	25.4	16	1	AR577635	ACCESSION:AR577635
C	40	15	25.4	16	1	AR577636	ACCESSION:AR577636
	41	14	23.7	15	1	BD178521	ACCESSION:BD178521
	42	14	23.7	15	1	BD178522	ACCESSION:BD178522
	43	14	23.7	15	1	BD178523	ACCESSION:BD178523
	44	14	23.7	15	1	BD178524	ACCESSION:BD178524
	45	14	23.7	15	1	BD182914	ACCESSION:BD182914
	46	14	23.7	15	1	BD182915	ACCESSION:BD182915
	47	14	23.7	15	1	BD182916	ACCESSION:BD182916
	48	14	23.7	15	1	BD182917	ACCESSION:BD182917
C	49	12.8	21.7	16	1	BD266222	ACCESSION:BD266222
	50	12	20.3	15	1	AR285765	ACCESSION:AR285765
	51	12	20.3	15	1	AR397756	ACCESSION:AR397756
	52	11	18.6	13	1	AR285764	ACCESSION:AR285764
	53	11	18.6	13	1	AR397755	ACCESSION:AR397755
	54	10.4	17.6	12	1	AR199318	ACCESSION:AR199318
	55	10.4	17.6	12	1	AR218368	ACCESSION:AR218368

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 08:27:03 ; Search time 3766 Seconds
 (without alignments)
 7218.081 Million cell updates/sec

Title: US-10-633-659-1
 Perfect score: 580.6
 Sequence: 1 atgagccagactccagggag.....ccagcactgcgcagggaccg 581

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_est3:*
 4: gb_htc:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_est7:*
 9: gb_gss1:*
 10: gb_gss2:*
 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	129.2	22.3	516	6 CB151486	CB151486 K-EST0208
2	82.8	14.3	1099	3 BM542919	BM542919 AGENCOURT
3	80.4	13.8	581	3 BP357610	BP357610 BP357610
4	80.2	13.8	583	3 BP352876	BP352876 BP352876
5	79.6	13.7	584	3 BP288529	BP288529 BP288529
6	79.4	13.7	582	3 BP287917	BP287917 BP287917

	7	78.4	13.5	582	3	BP288347	BP288347	BP288347
	8	78.4	13.5	662	1	AU122500	AU122500	AU122500
	9	76.8	13.2	582	3	BP227098	BP227098	BP227098
	10	76.8	13.2	758	5	BU502422	BU502422	AGENCOURT
	11	73.6	12.7	300	1	AU098655	AU098655	AU098655
	12	72.8	12.5	912	5	BQ722469	BQ722469	AGENCOURT
	13	70.8	12.2	837	5	BU521726	BU521726	AGENCOURT
	14	62.8	10.8	559	2	BF971481	BF971481	602239710
	15	62.8	10.8	740	3	BI910353	BI910353	603068006
	16	62.8	10.8	875	2	BG339685	BG339685	602437261
	17	62.8	10.8	927	2	BG339205	BG339205	602437061
	18	61.2	10.5	410	6	CD709587	CD709587	EST26114
	19	55.8	9.6	387	1	AV687113	AV687113	AV687113
	20	55.8	9.6	897	5	BQ722693	BQ722693	AGENCOURT
	21	51.4	8.9	841	1	AU121592	AU121592	AU121592
	22	47.8	8.2	581	3	BP286410	BP286410	BP286410
	23	47.2	8.1	925	10	CNS0091P	AL053013	Drosophil
	24	47	8.1	1464	3	BM918053	BM918053	AGENCOURT
	25	46	7.9	678	3	BI461755	BI461755	603202410
	26	45.6	7.9	682	10	CL150613	CL150613	104_332_1
C	27	45.6	7.9	749	10	CL150614	CL150614	104_332_1
	28	45.4	7.8	619	7	CV574281	CV574281	oe22d10.y
	29	45.2	7.8	389	1	AV690457	AV690457	AV690457
C	30	44.8	7.7	964	10	CNS003WG	AL065254	Drosophil
	31	44.4	7.6	1067	9	BZ052137	BZ052137	jnr70b01.
	32	44.2	7.6	931	1	AL583415	AL583415	AL583415
	33	44	7.6	1450	8	DN721093	DN721093	CNB137-E0
C	34	43.6	7.5	839	10	CNS004NB	AL054280	Drosophil
	35	43	7.4	942	5	BX447962	BX447962	BX447962
	36	43	7.4	951	1	AL559041	AL559041	AL559041
	37	42.8	7.4	770	9	AQ584491	AQ584491	RPCI-11-4
	38	42.8	7.4	807	9	CC488057	CC488057	CH240_319
C	39	42.6	7.3	622	9	CE020982	CE020982	tigr-gss-
	40	42	7.2	554	10	AG008555	AG008555	Homo sapi
	41	42	7.2	686	10	AG007239	AG007239	Homo sapi
	42	41.8	7.2	738	10	CNS015ST	AL105863	Drosophil
	43	41.6	7.2	683	10	AG007238	AG007238	Homo sapi
	44	41.6	7.2	895	10	CZ274878	CZ274878	ZMMBF0056
C	45	41.4	7.1	589	9	AZ996598	AZ996598	2M0282P13

OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 09:31:00 ; Search time 370 Seconds
 (without alignments)
 3661.408 Million cell updates/sec

Title: US-10-633-659-1
 Perfect score: 580.6
 Sequence: 1 atgagccagactccagggag.....ccagcactgcgcagggaccg 581

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_New:*
 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
 7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	41.6	7.2	1192	6	US-09-925-065A-700785	Sequence 700785,
2	39.4	6.8	600	6	US-09-925-065A-783232	Sequence 783232,
c 3	39	6.7	601	6	US-09-925-065A-503440	Sequence 503440,
4	39	6.7	619	6	US-09-925-065A-770564	Sequence 770564,
5	39	6.7	619	6	US-09-925-065A-770565	Sequence 770565,

	6	39	6.7	619	6	US-09-925-065A-770566	Sequence 770566,
c	7	39	6.7	1802	6	US-09-925-065A-675656	Sequence 675656,
c	8	39	6.7	1802	6	US-09-925-065A-675657	Sequence 675657,
	9	38.4	6.6	744	6	US-09-925-065A-75796	Sequence 75796, A
	10	38.2	6.6	570	6	US-09-925-065A-799662	Sequence 799662,
	11	38.2	6.6	570	6	US-09-925-065A-853637	Sequence 853637,
	12	38.2	6.6	633	6	US-09-925-065A-917678	Sequence 917678,
	13	38.2	6.6	633	6	US-09-925-065A-917679	Sequence 917679,
c	14	38	6.5	604	6	US-09-925-065A-609550	Sequence 609550,
c	15	38	6.5	628	6	US-09-925-065A-526372	Sequence 526372,
c	16	37.8	6.5	29584	7	US-10-330-773-612	Sequence 612, App
c	17	37.6	6.5	1046	8	US-10-750-185-57318	Sequence 57318, A
c	18	37.6	6.5	1046	8	US-10-750-623-57318	Sequence 57318, A
	19	37.4	6.4	905	6	US-09-925-065A-70317	Sequence 70317, A
	20	37.4	6.4	905	6	US-09-925-065A-70318	Sequence 70318, A
	21	37.4	6.4	905	6	US-09-925-065A-70319	Sequence 70319, A
	22	37.4	6.4	905	6	US-09-925-065A-70320	Sequence 70320, A
	23	37.4	6.4	905	6	US-09-925-065A-70321	Sequence 70321, A
	24	37	6.4	285	6	US-09-925-065A-484586	Sequence 484586,
	25	37	6.4	651	6	US-09-925-065A-876677	Sequence 876677,
	26	37	6.4	651	6	US-09-925-065A-905822	Sequence 905822,
c	27	36.8	6.3	528	6	US-09-925-065A-460511	Sequence 460511,
c	28	36.8	6.3	528	6	US-09-925-065A-460512	Sequence 460512,
	29	36.4	6.3	620	6	US-09-925-065A-93045	Sequence 93045, A
	30	36.4	6.3	1088	6	US-09-925-065A-550763	Sequence 550763,
	31	36.4	6.3	1291	8	US-10-750-185-42709	Sequence 42709, A
	32	36.4	6.3	1291	8	US-10-750-623-42709	Sequence 42709, A
c	33	36.4	6.3	7450	12	US-11-124-367A-103	Sequence 103, App
c	34	36.4	6.3	9630	12	US-11-124-367A-102	Sequence 102, App
	35	36.4	6.3	246960	12	US-11-121-086-8	Sequence 8, Appli
	36	36.2	6.2	525	6	US-09-925-065A-877450	Sequence 877450,
c	37	36.2	6.2	628	6	US-09-925-065A-799476	Sequence 799476,
c	38	36.2	6.2	630	6	US-09-925-065A-764864	Sequence 764864,
c	39	36.2	6.2	630	6	US-09-925-065A-831977	Sequence 831977,
c	40	36	6.2	463	6	US-09-925-065A-783195	Sequence 783195,
	41	36	6.2	485	6	US-09-925-065A-149786	Sequence 149786,
c	42	36	6.2	558	6	US-09-925-065A-469258	Sequence 469258,
	43	36	6.2	612	6	US-09-925-065A-802945	Sequence 802945,
	44	36	6.2	612	6	US-09-925-065A-856429	Sequence 856429,
	45	35.8	6.2	1846	8	US-10-750-185-59483	Sequence 59483, A

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 08:36:13 ; Search time 874 Seconds
(without alignments)
5497.149 Million cell updates/sec

Title: US-10-633-659-1
Perfect score: 580.6
Sequence: 1 atgagccagactccagggag.....ccagcactgcgcagggaccg 581

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	580.6	100.0	581	3	US-09-813-031-1
2	580.6	100.0	581	3	US-09-813-990A-1
3	580.6	100.0	581	9	US-10-633-659-1
4	580	100.0	581	7	US-10-070-415A-16
5	579.6	99.8	581	7	US-10-070-415A-39
6	579.6	99.8	581	7	US-10-070-415A-40
7	579	99.7	581	3	US-09-813-031-2
8	579	99.7	581	3	US-09-813-031-3

	9	579	99.7	581	3	US-09-813-031-4	Sequence 4, Appli
	10	579	99.7	581	3	US-09-813-990A-2	Sequence 2, Appli
	11	579	99.7	581	3	US-09-813-990A-3	Sequence 3, Appli
	12	579	99.7	581	3	US-09-813-990A-4	Sequence 4, Appli
	13	579	99.7	581	9	US-10-633-659-2	Sequence 2, Appli
	14	579	99.7	581	9	US-10-633-659-3	Sequence 3, Appli
	15	579	99.7	581	9	US-10-633-659-4	Sequence 4, Appli
	16	578.4	99.6	581	7	US-10-070-415A-17	Sequence 17, Appl
	17	578.4	99.6	581	7	US-10-070-415A-18	Sequence 18, Appl
	18	578.4	99.6	581	7	US-10-070-415A-19	Sequence 19, Appl
	19	578.4	99.6	581	7	US-10-070-415A-37	Sequence 37, Appl
	20	578.4	99.6	581	7	US-10-070-415A-38	Sequence 38, Appl
	21	518.6	89.3	5376	8	US-10-492-396-7	Sequence 7, Appli
	22	461	79.4	2451	8	US-10-492-396-5	Sequence 5, Appli
	23	388.2	66.9	5981	6	US-10-311-455-2165	Sequence 2165, Ap
c	24	277.4	47.8	5981	6	US-10-311-455-2166	Sequence 2166, Ap
	25	122	21.0	150	3	US-09-813-990A-23	Sequence 23, Appl
c	26	106.8	18.4	121	9	US-10-239-175-1	Sequence 1, Appli
	27	104.4	18.0	549	8	US-10-492-396-6	Sequence 6, Appli
c	28	91.8	15.8	5284	6	US-10-247-671-90	Sequence 90, Appl
	29	91.4	15.7	2855	5	US-10-044-090-540	Sequence 540, App
c	30	44.2	7.6	189	3	US-09-854-867-194	Sequence 194, App
c	31	44.2	7.6	189	9	US-10-786-970A-194	Sequence 194, App
	32	41.6	7.2	1192	4	US-09-925-065A-700785	Sequence 700785,
	33	41.2	7.1	882	5	US-10-184-644-574	Sequence 574, App
	34	41.2	7.1	882	5	US-10-184-634-574	Sequence 574, App
c	35	41	7.1	446	5	US-10-106-698-2185	Sequence 2185, Ap
	36	39.4	6.8	600	4	US-09-925-065A-783232	Sequence 783232,
c	37	39.4	6.8	1058	5	US-10-027-632-100842	Sequence 100842,
c	38	39.4	6.8	1058	5	US-10-027-632-100843	Sequence 100843,
c	39	39.4	6.8	1058	6	US-10-027-632-100842	Sequence 100842,
c	40	39.4	6.8	1058	6	US-10-027-632-100843	Sequence 100843,
c	41	39	6.7	601	4	US-09-925-065A-503440	Sequence 503440,
	42	39	6.7	619	4	US-09-925-065A-770564	Sequence 770564,
	43	39	6.7	619	4	US-09-925-065A-770565	Sequence 770565,
	44	39	6.7	619	4	US-09-925-065A-770566	Sequence 770566,
	45	39	6.7	1248	5	US-10-027-632-124870	Sequence 124870,

OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 08:31:48 ; Search time 174 Seconds
 (without alignments)
 5935.421 Million cell updates/sec

Title: US-10-633-659-1
 Perfect score: 580.6
 Sequence: 1 atgagccagactccagggag.....ccagcactgcgcagggaccg 581

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	580.6	100.0	581	3	US-09-813-031-1	Sequence 1, Appli
2	580.6	100.0	581	3	US-09-813-990A-1	Sequence 1, Appli
3	579	99.7	581	3	US-09-813-031-2	Sequence 2, Appli
4	579	99.7	581	3	US-09-813-031-3	Sequence 3, Appli
5	579	99.7	581	3	US-09-813-031-4	Sequence 4, Appli
6	579	99.7	581	3	US-09-813-990A-2	Sequence 2, Appli
7	579	99.7	581	3	US-09-813-990A-3	Sequence 3, Appli
8	579	99.7	581	3	US-09-813-990A-4	Sequence 4, Appli
9	122	21.0	150	3	US-09-813-990A-23	Sequence 23, Appli

	10	58.6	10.1	134	3	US-09-513-999C-18706	Sequence 18706, A
c	11	52.2	9.0	7218	2	US-08-232-463-14	Sequence 14, Appl
c	12	44.2	7.6	189	3	US-09-573-080A-194	Sequence 194, App
c	13	40.6	7.0	7381	3	US-09-949-016-16844	Sequence 16844, A
	14	40.2	6.9	39601	3	US-09-949-016-16045	Sequence 16045, A
c	15	39.4	6.8	148783	3	US-09-949-016-15729	Sequence 15729, A
c	16	38.6	6.6	163662	3	US-09-949-016-12545	Sequence 12545, A
c	17	38.6	6.6	163664	3	US-09-949-016-13546	Sequence 13546, A
	18	38.2	6.6	601	3	US-09-949-016-33664	Sequence 33664, A
	19	38.2	6.6	601	3	US-09-949-016-62504	Sequence 62504, A
	20	38.2	6.6	601	3	US-09-949-016-105623	Sequence 105623,
	21	38.2	6.6	601	3	US-09-949-016-105625	Sequence 105625,
	22	38.2	6.6	601	3	US-09-949-016-105626	Sequence 105626,
	23	38.2	6.6	129899	3	US-09-949-016-14684	Sequence 14684, A
	24	38.2	6.6	148156	3	US-09-949-016-11776	Sequence 11776, A
c	25	38.2	6.6	524032	3	US-09-949-016-16928	Sequence 16928, A
c	26	38.2	6.6	524032	3	US-09-949-016-16929	Sequence 16929, A
c	27	38.2	6.6	524032	3	US-09-949-016-16930	Sequence 16930, A
c	28	38.2	6.6	524032	3	US-09-949-016-16931	Sequence 16931, A
c	29	38.2	6.6	529885	3	US-09-949-016-14340	Sequence 14340, A
c	30	38.2	6.6	529885	3	US-09-949-016-14341	Sequence 14341, A
c	31	38.2	6.6	529885	3	US-09-949-016-14342	Sequence 14342, A
c	32	38.2	6.6	529885	3	US-09-949-016-14343	Sequence 14343, A
c	33	38.2	6.6	529885	3	US-09-949-016-14344	Sequence 14344, A
c	34	38.2	6.6	529885	3	US-09-949-016-14345	Sequence 14345, A
c	35	38.2	6.6	529885	3	US-09-949-016-14346	Sequence 14346, A
c	36	38.2	6.6	529885	3	US-09-949-016-14347	Sequence 14347, A
	37	37.8	6.5	601	3	US-09-949-016-105624	Sequence 105624,
	38	37.6	6.5	75674	3	US-09-949-016-17597	Sequence 17597, A
c	39	37.4	6.4	54270	3	US-09-949-016-16096	Sequence 16096, A
c	40	37.4	6.4	76164	3	US-09-949-016-12288	Sequence 12288, A
c	41	37.4	6.4	76165	3	US-09-949-016-14005	Sequence 14005, A
	42	37.2	6.4	16350	3	US-09-902-540-1144	Sequence 1144, Ap
c	43	37.2	6.4	193303	3	US-09-497-855A-37	Sequence 37, Appl
c	44	37.2	6.4	193303	3	US-09-497-855A-44	Sequence 44, Appl
c	45	37	6.4	1243	3	US-09-322-357-63	Sequence 63, Appl

OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 08:25:20 ; Search time 526 Seconds
 (without alignments)
 7361.571 Million cell updates/sec

Title: US-10-633-659-1
 Perfect score: 580.6
 Sequence: 1 atgagccagactccagggag.....ccagcactgcgcagggaccg 581

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_21:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	580.6	100.0	581	4	AAI70373	Aai70373 Human MxA
2	580.6	100.0	581	5	AAI70350	Aai70350 Promoter
3	580	100.0	581	10	ABX08682	Abx08682 Pathogeni
4	579.6	99.8	581	10	ABX08706	Abx08706 Pathogeni

	5	579.6	99.8	581	10	ABX08705	Abx08705 Pathogeni
	6	579.6	99.8	581	12	ADL92270	Adl92270 Human MxA
	7	579	99.7	581	4	AAI70375	Aai70375 Human MxA
	8	579	99.7	581	4	AAI70376	Aai70376 Human MxA
	9	579	99.7	581	4	AAI70374	Aai70374 Human MxA
	10	579	99.7	581	5	AAI70353	Aai70353 Promoter
	11	579	99.7	581	5	AAI70352	Aai70352 Promoter
	12	579	99.7	581	5	AAI70351	Aai70351 Promoter
	13	578.4	99.6	581	10	ABX08704	Abx08704 Pathogeni
	14	578.4	99.6	581	10	ABX08685	Abx08685 Pathogeni
	15	578.4	99.6	581	10	ABX08703	Abx08703 Pathogeni
	16	578.4	99.6	581	10	ABX08683	Abx08683 Pathogeni
	17	578.4	99.6	581	10	ABX08684	Abx08684 Pathogeni
	18	578.4	99.6	581	12	ADL92263	Adl92263 Human MxA
	19	578.4	99.6	581	12	ADL92264	Adl92264 Human MxA
	20	578	99.6	581	12	ADL92269	Adl92269 Human MxA
	21	576.8	99.3	581	12	ADL92267	Adl92267 Human MxA
	22	576.8	99.3	581	12	ADL92266	Adl92266 Human MxA
	23	576.8	99.3	581	12	ADL92265	Adl92265 Human MxA
	24	576.8	99.3	581	12	ADL92268	Adl92268 Human MxA
	25	565.4	97.4	49343	14	AEB96544	Aeb96544 Human MX1
	26	518.6	89.3	5376	9	AAD55995	Aad55995 Luciferas
	27	461	79.4	2451	9	AAD55993	Aad55993 Human MxA
	28	388.2	66.9	5981	6	ABL34192	Abl34192 Human imm
	29	388.2	66.9	5981	6	ABL70483	Abl70483 Chemicall
c	30	277.4	47.8	5981	6	ABL34193	Abl34193 Human imm
c	31	277.4	47.8	5981	6	ABL70484	Abl70484 Chemicall
c	32	131.8	22.7	238	13	ADT02368	Adt02368 Target nu
c	33	131.6	22.7	132	12	ADO78057	Ado78057 Human MxA
c	34	131.6	22.7	132	12	ADO78056	Ado78056 Human MxA
	35	118	20.3	149	4	AAI70395	Aai70395 Human MxA
	36	118	20.3	149	5	AAI70372	Aai70372 Promoter
	37	108.6	18.7	241	14	ADY97400	Ady97400 Target nu
c	38	108.4	18.7	121	12	ADO78063	Ado78063 Human MxA
	39	108.4	18.7	121	14	ADW92011	Adw92011 Amplified
	40	108.4	18.7	121	14	ADZ58674	Adz58674 Novel exi
c	41	106.8	18.4	121	12	ADL72194	Adl72194 Human nuc
c	42	106.8	18.4	121	12	ADO78062	Ado78062 Human MxA
	43	106.8	18.4	121	14	ADW92010	Adw92010 Amplified
	44	106.8	18.4	121	14	ADY97398	Ady97398 Target nu
	45	106.8	18.4	121	14	ADZ58673	Adz58673 Novel exi

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 08:26:45 ; Search time 4559 Seconds
(without alignments)
7244.142 Million cell updates/sec

Title: US-10-633-659-1
Perfect score: 580.6
Sequence: 1 atgagccagactccagggag.....ccagcactgcgcagggaccg 581

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	580.6	100.0	581	6	BD090451	BD090451 Carrier f
2	580.6	100.0	581	6	BD090746	BD090746 Polymorph
3	580.6	100.0	581	6	AR441761	AR441761 Sequence

	4	580.6	100.0	581	6	AR577621	AR577621	Sequence
	5	580	100.0	581	6	BD178510	BD178510	Method of
	6	580	100.0	581	6	BD182903	BD182903	Detection
	7	579.6	99.8	581	6	BD178533	BD178533	Method of
	8	579.6	99.8	581	6	BD178534	BD178534	Method of
	9	579.6	99.8	581	6	BD182926	BD182926	Detection
	10	579.6	99.8	581	6	BD182927	BD182927	Detection
	11	579	99.7	581	6	BD090452	BD090452	Carrier f
	12	579	99.7	581	6	BD090453	BD090453	Carrier f
	13	579	99.7	581	6	BD090454	BD090454	Carrier f
	14	579	99.7	581	6	BD090747	BD090747	Polymorph
	15	579	99.7	581	6	BD090748	BD090748	Polymorph
	16	579	99.7	581	6	BD090749	BD090749	Polymorph
	17	579	99.7	581	6	AR441762	AR441762	Sequence
	18	579	99.7	581	6	AR441763	AR441763	Sequence
	19	579	99.7	581	6	AR441764	AR441764	Sequence
	20	579	99.7	581	6	AR577622	AR577622	Sequence
	21	579	99.7	581	6	AR577623	AR577623	Sequence
	22	579	99.7	581	6	AR577624	AR577624	Sequence
	23	578.4	99.6	581	6	BD178511	BD178511	Method of
	24	578.4	99.6	581	6	BD178512	BD178512	Method of
	25	578.4	99.6	581	6	BD178513	BD178513	Method of
	26	578.4	99.6	581	6	BD178531	BD178531	Method of
	27	578.4	99.6	581	6	BD178532	BD178532	Method of
	28	578.4	99.6	581	6	BD182904	BD182904	Detection
	29	578.4	99.6	581	6	BD182905	BD182905	Detection
	30	578.4	99.6	581	6	BD182906	BD182906	Detection
	31	578.4	99.6	581	6	BD182924	BD182924	Detection
	32	578.4	99.6	581	6	BD182925	BD182925	Detection
c	33	565.4	97.4	3339	8	HUM8DC6Z	L35661	Homo sapien
	34	565.4	97.4	4341	6	CS124352	CS124352	Sequence
	35	565.4	97.4	40100	8	HS25D2	AL773576	Homo sapi
	36	565.4	97.4	41120	8	HS14C10	AL773577	Homo sapi
	37	565.4	97.4	60904	8	AC005612	AC005612	Homo sapi
	38	565.4	97.4	340000	8	HS21C085	AL163285	Homo sapi
	39	563.8	97.1	108927	8	AP001609	AP001609	Homo sapi
	40	555.8	95.7	212865	8	AL954241	AL954241	Pan trogl
	41	524.2	90.3	1899	8	HSMXAP	X55639	H.sapiens D
	42	388.2	66.9	4341	6	CS124594	CS124594	Sequence
	43	388.2	66.9	5981	6	AX347094	AX347094	Sequence
	44	388.2	66.9	5981	6	AX348915	AX348915	Sequence
	45	332.4	57.3	4341	6	CS124716	CS124716	Sequence

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 09:37:39 ; Search time 3079.5 Seconds
(without alignments)
227.896 Million cell updates/sec

Title: US-10-633-659-1_COPY_441_455
Perfect score: 15
Sequence: 1 ggtttcgtttctgct 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 94

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	15	100.0	128	7	CK910216	CK910216 e3fmg
c 2	15	100.0	163	6	CD012341	CD012341 VVC011D11
c 3	15	100.0	194	9	BH918850	BH918850 3526_1_62
4	15	100.0	201	6	CB005305	CB005305 VVC011D11
c 5	15	100.0	298	1	AV968305	AV968305 AV968305
c 6	15	100.0	307	1	AA509002	AA509002 MBAFCX6B0
7	15	100.0	336	5	BW516948	BW516948 BW516948

	8	15	100.0	354	1	AI647115	AI647115 vn15f04.y
c	9	15	100.0	376	1	AJ495045	AJ495045 AJ495045
	10	15	100.0	381	7	CO671586	CO671586 DG33-80n2
c	11	15	100.0	384	1	AJ494396	AJ494396 AJ494396
	12	15	100.0	410	6	CB348291	CB348291 CAB2SG000
	13	15	100.0	415	11	PT010A01R	AL448634 Parameciu
c	14	15	100.0	416	6	CB567143	CB567143 AGENCOURT
	15	15	100.0	420	5	BW491958	BW491958 BW491958
c	16	15	100.0	422	6	CB348364	CB348364 CAB2SG000
c	17	15	100.0	424	7	CN548430	CN548430 EST 16068
	18	15	100.0	431	1	AA636196	AA636196 vn15f04.r
c	19	15	100.0	444	1	AJ495121	AJ495121 AJ495121
c	20	15	100.0	454	10	CL382271	CL382271 RPCI44_32
	21	15	100.0	463	2	BF443134	BF443134 260511 MA
	22	15	100.0	468	5	BW587980	BW587980 BW587980
	23	15	100.0	488	8	DR997202	DR997202 Mdfb8003E
	24	15	100.0	494	10	CG227200	CG227200 OGVCQ38TH
c	25	15	100.0	550	9	CC953003	CC953003 BOIHA66TR
	26	15	100.0	552	6	CF349924	CF349924 fc2805.e
c	27	15	100.0	572	7	CN444700	CN444700 Mdfw2003h
	28	15	100.0	585	5	BW517417	BW517417 BW517417
	29	15	100.0	595	6	CB910353	CB910353 VVD177B04
	30	15	100.0	596	10	CL360828	CL360828 RPCI44_34
	31	15	100.0	604	6	CA991500	CA991500 HC0422 GI
c	32	15	100.0	610	5	BW344740	BW344740 BW344740
c	33	15	100.0	625	5	BW341585	BW341585 BW341585
c	34	15	100.0	626	5	BW238664	BW238664 BW238664
c	35	15	100.0	628	1	AV674788	AV674788 AV674788
c	36	15	100.0	650	7	CN153416	CN153416 940529 MA
	37	15	100.0	650	7	CN155529	CN155529 942833 MA
c	38	15	100.0	651	7	CV173141	CV173141 dba32f06.
c	39	15	100.0	657	5	BW344529	BW344529 BW344529
c	40	15	100.0	661	3	BP513630	BP513630 BP513630
	41	15	100.0	670	7	CV093265	CV093265 FAMU_USDA
c	42	15	100.0	674	10	CZ782755	CZ782755 OC_Ba014
c	43	15	100.0	678	9	BZ029324	BZ029324 oeh11e10.
c	44	15	100.0	680	5	BW241814	BW241814 BW241814
c	45	15	100.0	684	5	BW248663	BW248663 BW248663
c	46	15	100.0	685	5	BW355596	BW355596 BW355596
c	47	15	100.0	685	8	DN119798	DN119798 1119753 M
c	48	15	100.0	688	5	BW350001	BW350001 BW350001
	49	15	100.0	688	8	DT024265	DT024265 VVI120A08
c	50	15	100.0	692	1	AV970752	AV970752 AV970752
c	51	15	100.0	699	5	BW346883	BW346883 BW346883
c	52	15	100.0	700	5	BW241899	BW241899 BW241899
	53	15	100.0	700	6	CF363544	CF363544 833432 MA
c	54	15	100.0	709	9	BZ035386	BZ035386 oeh99c02.
c	55	15	100.0	710	7	CO480574	CO480574 GQ0162.TB
c	56	15	100.0	711	5	BW238785	BW238785 BW238785
c	57	15	100.0	719	5	BW348329	BW348329 BW348329
	58	15	100.0	720	3	BP796101	BP796101 BP796101
	59	15	100.0	721	9	CC949169	CC949169 BOIGD40TR
	60	15	100.0	725	3	BP143478	BP143478 BP143478
c	61	15	100.0	737	6	CB971098	CB971098 CAB10004_
	62	15	100.0	745	5	BW409799	BW409799 BW409799
	63	15	100.0	746	5	BW110816	BW110816 BW110816
c	64	15	100.0	749	10	CZ693884	CZ693884 OC_Ba000

	65	15	100.0	757	6	CB971178	CB971178	CAB10004_
	66	15	100.0	758	11	CR867988	CR867988	Sus scrOf
c	67	15	100.0	760	5	BW429474	BW429474	BW429474
	68	15	100.0	763	5	BW499091	BW499091	BW499091
	69	15	100.0	778	5	BW402350	BW402350	BW402350
	70	15	100.0	781	5	BW398836	BW398836	BW398836
	71	15	100.0	784	5	BW098086	BW098086	BW098086
	72	15	100.0	788	6	CF512719	CF512719	CABud0004
	73	15	100.0	790	9	BH695991	BH695991	BOHYV91TF
	74	15	100.0	810	9	BH210907	BH210907	Sm1-51D1.
c	75	15	100.0	814	3	BI647545	BI647545	603278124
c	76	15	100.0	818	8	CX894301	CX894301	JGI_CAAM5
	77	15	100.0	819	5	BW496996	BW496996	BW496996
c	78	15	100.0	831	5	BW969016	BW969016	BW969016
c	79	15	100.0	838	1	AL667445	AL667445	AL667445
	80	15	100.0	850	10	CW983040	CW983040	KBrH008E0
c	81	15	100.0	889	8	CX912562	CX912562	JGI_CAAN3
	82	15	100.0	898	1	AL665250	AL665250	AL665250
c	83	15	100.0	900	1	AL668316	AL668316	AL668316
c	84	15	100.0	905	9	BZ133002	BZ133002	CH230-346
c	85	15	100.0	918	2	BF101998	BF101998	601752966
	86	15	100.0	926	10	CG137706	CG137706	PUFOB03TB
c	87	15	100.0	936	10	CG137708	CG137708	PUFOB03TD
c	88	15	100.0	972	11	CNS06GG7	AL397661	T3 end of
c	89	15	100.0	978	10	AG136188	AG136188	Pan trogl
	90	15	100.0	1053	5	BX838578	BX838578	BX838578
c	91	15	100.0	1094	2	BF314647	BF314647	601900678
c	92	15	100.0	1231	2	BF688791	BF688791	602184970
c	93	15	100.0	1343	8	DN476019	DN476019	altr202xo
	94	15	100.0	1849	4	CNS0AC88	BX814013	Arabidops

OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 09:49:03 ; Search time 1002.5 Seconds
(without alignments)
34.888 Million cell updates/sec

Title: US-10-633-659-1_COPY_441_455
Perfect score: 15
Sequence: 1 ggtttcgtttctgct 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description

No matches found						

Search completed: March 22, 2006, 11:02:13

Job time : 1002.5 secs

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 09:41:42 ; Search time 354.5 Seconds
(without alignments)
349.903 Million cell updates/sec

Title: US-10-633-659-1_COPY_441_455
Perfect score: 15
Sequence: 1 ggtttcgtttctgct 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 24

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
c	1	15	100.0	16	3	US-09-813-031-5
	2	15	100.0	16	3	US-09-813-031-13
	3	15	100.0	16	3	US-09-813-990A-5
c	4	15	100.0	16	3	US-09-813-990A-13
	5	15	100.0	16	9	US-10-633-659-5
c	6	15	100.0	16	9	US-10-633-659-13
	7	15	100.0	539	5	US-10-027-632-219280
	8	15	100.0	539	5	US-10-027-632-219281

	9	15	100.0	539	5	US-10-027-632-219282	Sequence 219282,
	10	15	100.0	539	5	US-10-027-632-219283	Sequence 219283,
	11	15	100.0	539	6	US-10-027-632-219280	Sequence 219280,
	12	15	100.0	539	6	US-10-027-632-219281	Sequence 219281,
	13	15	100.0	539	6	US-10-027-632-219282	Sequence 219282,
	14	15	100.0	539	6	US-10-027-632-219283	Sequence 219283,
c	15	15	100.0	564	8	US-10-425-115-156980	Sequence 156980,
	16	15	100.0	581	3	US-09-813-031-1	Sequence 1, Appli
	17	15	100.0	581	3	US-09-813-990A-1	Sequence 1, Appli
	18	15	100.0	581	7	US-10-070-415A-16	Sequence 16, Appl
	19	15	100.0	581	9	US-10-633-659-1	Sequence 1, Appli
	20	15	100.0	600	9	US-10-972-079-36465	Sequence 36465, A
	21	15	100.0	1257	6	US-10-369-493-43293	Sequence 43293, A
c	22	15	100.0	1569	3	US-09-938-842A-3879	Sequence 3879, Ap
c	23	15	100.0	1569	3	US-09-938-842A-3879	Sequence 3879, Ap
	24	15	100.0	5376	8	US-10-492-396-7	Sequence 7, Appli

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 09:34:33 ; Search time 400.75 Seconds
(without alignments)
249.458 Million cell updates/sec

Title: US-10-633-659-1_COPY_441_455
Perfect score: 15
Sequence: 1 gggtttcgtttctgct 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 18

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 500 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query		DB	ID	Description
			Match	Length			
	1	15	100.0	16	4	AAI70377	Aai70377 Human MxA
c	2	15	100.0	16	4	AAI70385	Aai70385 MxA gene
	3	15	100.0	16	5	AAI70354	Aai70354 Human MxA
c	4	15	100.0	16	5	AAI70362	Aai70362 Human MxA

	5	15	100.0	120	14	ADY97399	Ady97399 Target nu
c	6	15	100.0	121	12	ADO78063	Ado78063 Human MxA
	7	15	100.0	121	14	ADW92011	Adw92011 Amplified
	8	15	100.0	121	14	ADZ58674	Adz58674 Novel exi
	9	15	100.0	241	14	ADY97400	Ady97400 Target nu
	10	15	100.0	581	4	AAI70373	Aai70373 Human MxA
	11	15	100.0	581	5	AAI70350	Aai70350 Promoter
	12	15	100.0	581	10	ABX08682	Abx08682 Pathogeni
	13	15	100.0	581	12	ADL92263	Adl92263 Human MxA
	14	15	100.0	1257	13	ADT44855	Adt44855 Bacterial
c	15	15	100.0	1569	6	ABZ16074	Abz16074 Arabidops
	16	15	100.0	5376	9	AAD55995	Aad55995 Luciferas
	17	15	100.0	110000	4	AAI99682_11	Continuation (12 o
	18	15	100.0	110000	4	AAI99683_11	Continuation (12 o

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 09:35:25 ; Search time 874 Seconds
(without alignments)
975.574 Million cell updates/sec

Title: US-10-633-659-1_COPY_441_455
Perfect score: 15
Sequence: 1 gggttcggtttctgct 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 55

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	16	6	BD090455	BD090455 Carrier f
c	2	15	100.0	16	6	BD090463	BD090463 Carrier f

	3	15	100.0	16	6	BD090750	BD090750 Polymorph
c	4	15	100.0	16	6	BD090758	BD090758 Polymorph
	5	15	100.0	16	6	AR441765	AR441765 Sequence
c	6	15	100.0	16	6	AR441773	AR441773 Sequence
	7	15	100.0	16	6	AR577625	AR577625 Sequence
c	8	15	100.0	16	6	AR577633	AR577633 Sequence
	9	15	100.0	581	6	BD090451	BD090451 Carrier f
	10	15	100.0	581	6	BD090746	BD090746 Polymorph
	11	15	100.0	581	6	BD178510	BD178510 Method of
	12	15	100.0	581	6	BD182903	BD182903 Detection
	13	15	100.0	581	6	AR441761	AR441761 Sequence
	14	15	100.0	581	6	AR577621	AR577621 Sequence
c	15	15	100.0	1569	6	AX509184	AX509184 Sequence
	16	15	100.0	2193	1	RLU44387	U44387 Rhizobium l
c	17	15	100.0	4902	2	AB048261	AB048261 Halocynth
	18	15	100.0	5263	1	RLRES	X98117 Rhizobium l
c	19	15	100.0	62282	14	AC135713	AC135713 Rattus no
c	20	15	100.0	101075	15	AC008030	AC008030 Arabidops
	21	15	100.0	110000	1	AE000516_11	Continuation (12 o
	22	15	100.0	110000	1	CR555306_10	Continuation (11 o
c	23	15	100.0	110000	14	CT005271_08	Continuation (9 of
c	24	15	100.0	110000	14	CT005271_09	Continuation (10 o
	25	15	100.0	139818	9	AC129309	AC129309 Mus muscu
	26	15	100.0	150600	14	CR847828	CR847828 Danio rer
c	27	15	100.0	151936	14	AC141791	AC141791 Apis mell
	28	15	100.0	165509	14	AC009886	AC009886 Homo sapi
	29	15	100.0	167099	5	BX950201	BX950201 Zebrafish
c	30	15	100.0	168614	8	AL357672	AL357672 Human DNA
	31	15	100.0	175019	5	BX901957	BX901957 Zebrafish
	32	15	100.0	176713	8	AP000751	AP000751 Homo sapi
	33	15	100.0	177071	14	AC128090	AC128090 Rattus no
	34	15	100.0	178942	8	AL357520	AL357520 Human DNA
	35	15	100.0	181401	14	AC146663	AC146663 Sus scrof
c	36	15	100.0	189747	14	AC087791	AC087791 Homo sapi
	37	15	100.0	190191	14	AC122368	AC122368 Mus muscu
c	38	15	100.0	192913	14	AP001265	AP001265 Homo sapi
c	39	15	100.0	200045	14	AC122678	AC122678 Rattus no
	40	15	100.0	200803	8	AC025580	AC025580 Homo sapi
	41	15	100.0	202209	9	AC140461	AC140461 Mus muscu
c	42	15	100.0	203223	14	AC127395	AC127395 Rattus no
c	43	15	100.0	207234	9	AC122263	AC122263 Mus muscu
c	44	15	100.0	214257	14	AC115562	AC115562 Rattus no
	45	15	100.0	219423	14	AC126093	AC126093 Rattus no
c	46	15	100.0	220817	14	AC112446	AC112446 Rattus no
	47	15	100.0	222603	14	AC125755	AC125755 Rattus no
	48	15	100.0	226736	9	AC098881	AC098881 Mus muscu
	49	15	100.0	241392	14	AC019279	AC019279 Homo sapi
	50	15	100.0	242596	14	AC120581	AC120581 Rattus no
	51	15	100.0	243490	14	AC131536	AC131536 Rattus no
c	52	15	100.0	245383	14	AL161653	AL161653 Homo sapi
c	53	15	100.0	298050	1	BX321861	BX321861 Nitrosomo
	54	15	100.0	327650	1	BX248337	BX248337 Mycobacte
	55	15	100.0	349306	1	BX842575	BX842575 Mycobacte